

Lane	1	2	3	4	5	6	7	8
Biotinylation	+	+	+	+	+	+	+	+
791T/36	+	-	+	-	+	-	+	-
1143/B7	-	+	-	+	-	+	-	+
DTSSP	-	-	+	+	-	-	+	+
Solubilisation	x	x	x	x	0	0	0	0

1 2 3 4 5 6 7 8

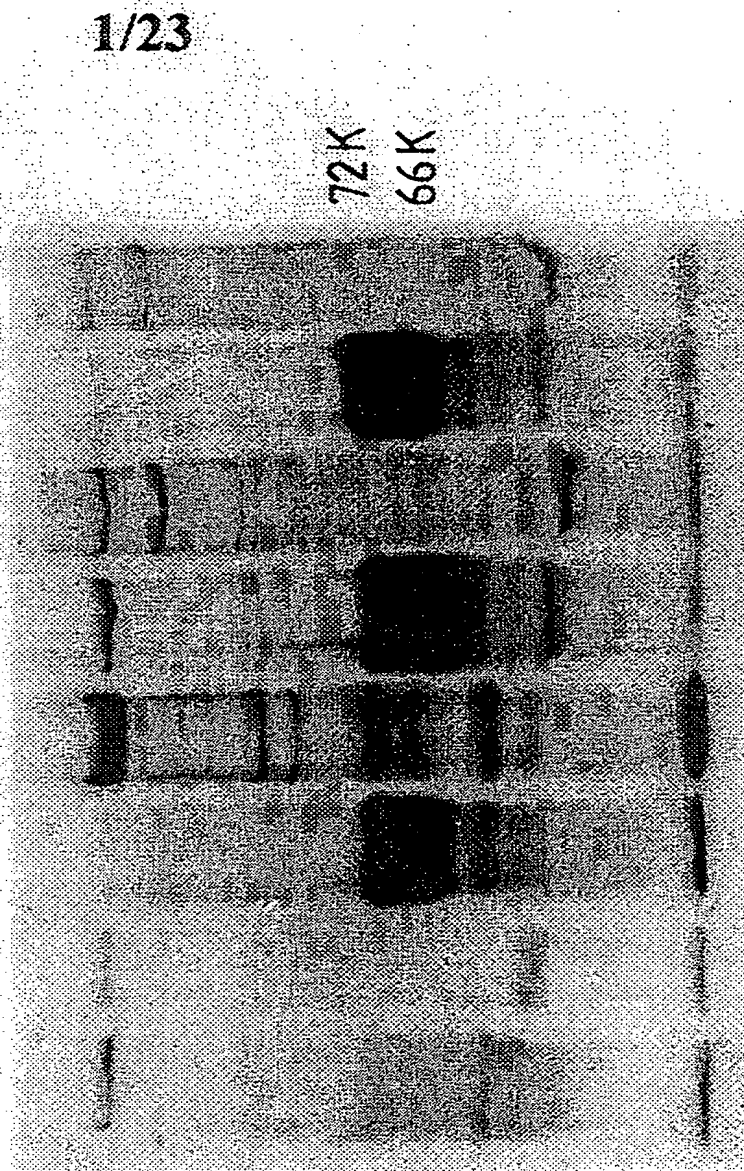


Fig. 1

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Detergent

Glucoside	+	-	-	-	-	-
NP-40	-	+	-	-	-	-
TX-100	-	-	+	+	+	+

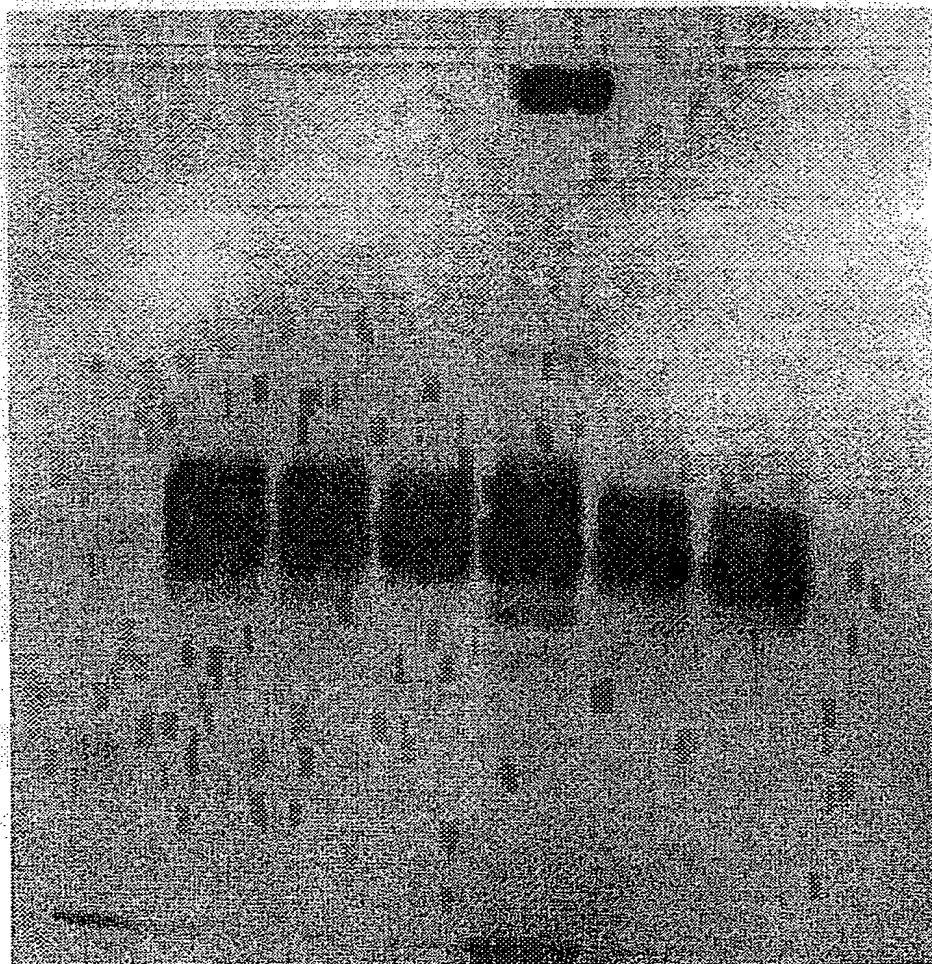
Centrifugation

13000 rpm	+	+	+	+	+	+
100,000 g	+	+	+	-	+	+
blue-2	-	-	-	-	+	+

97.4 K

66 K

45 K

**Fig. 2**

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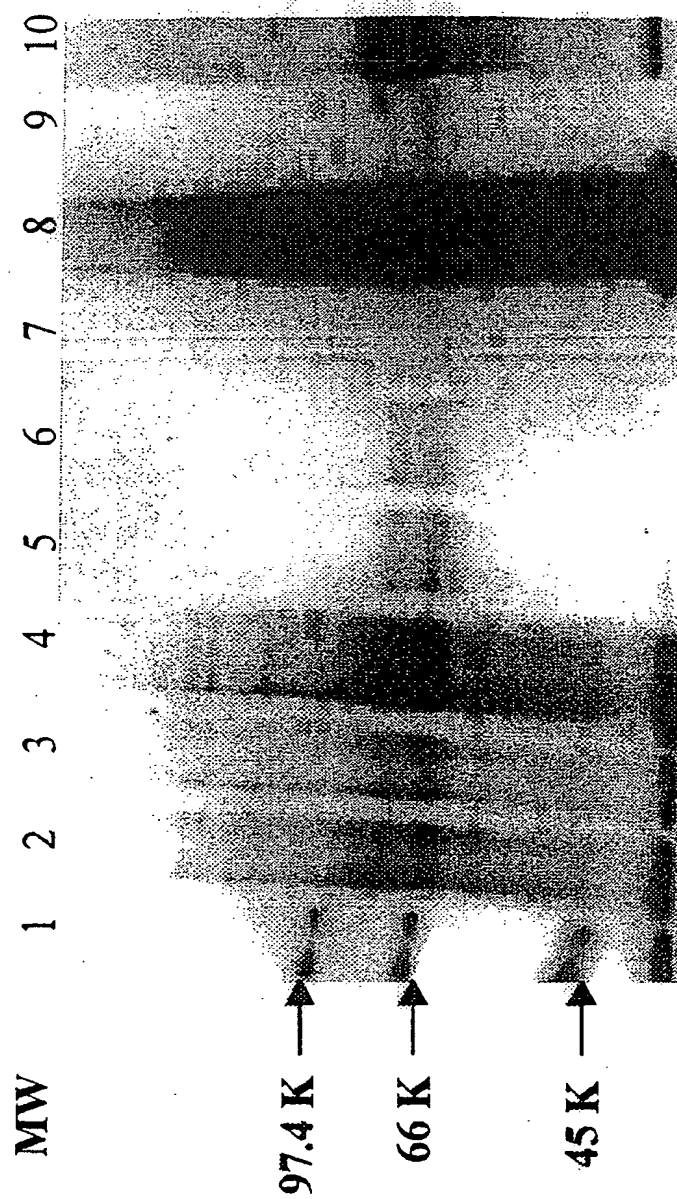


Fig. 3

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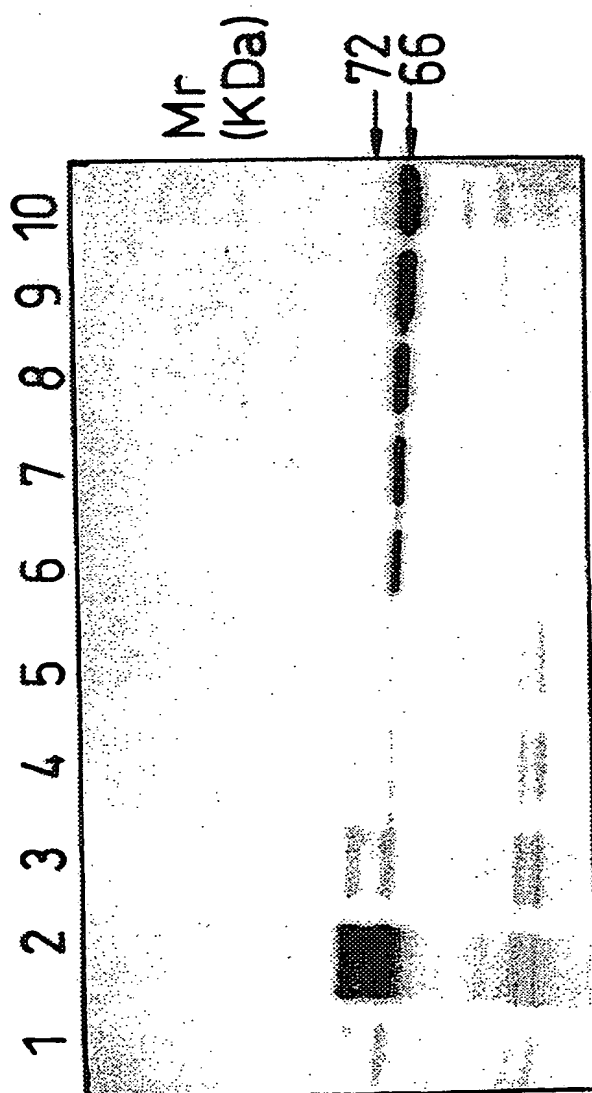


Fig. 4

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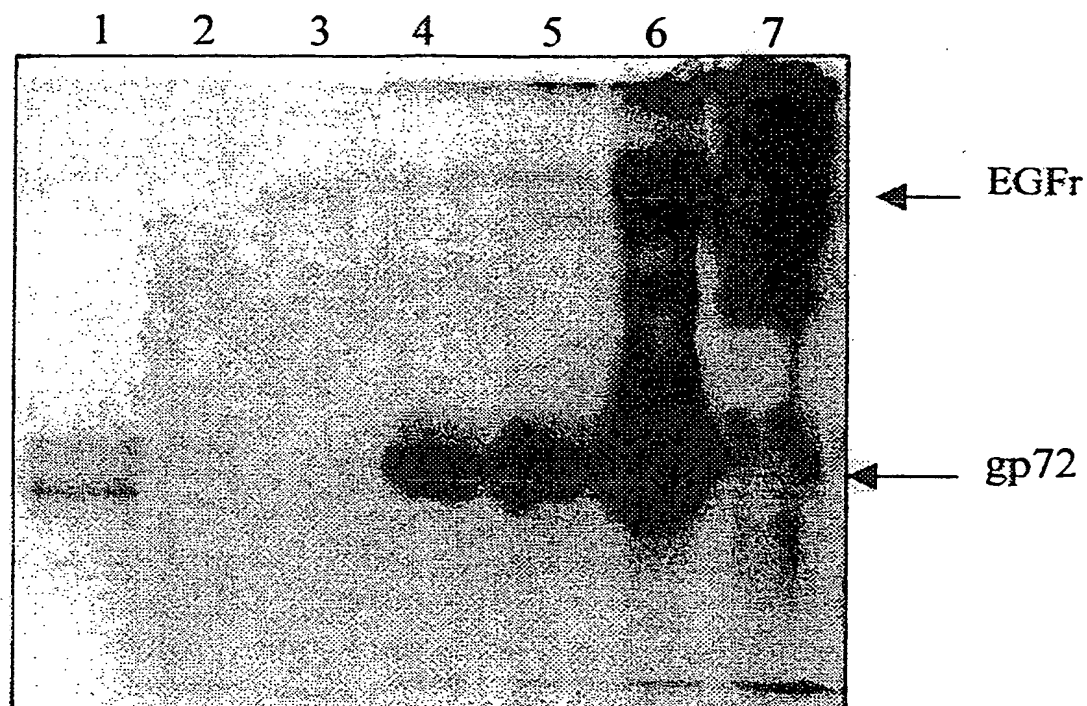
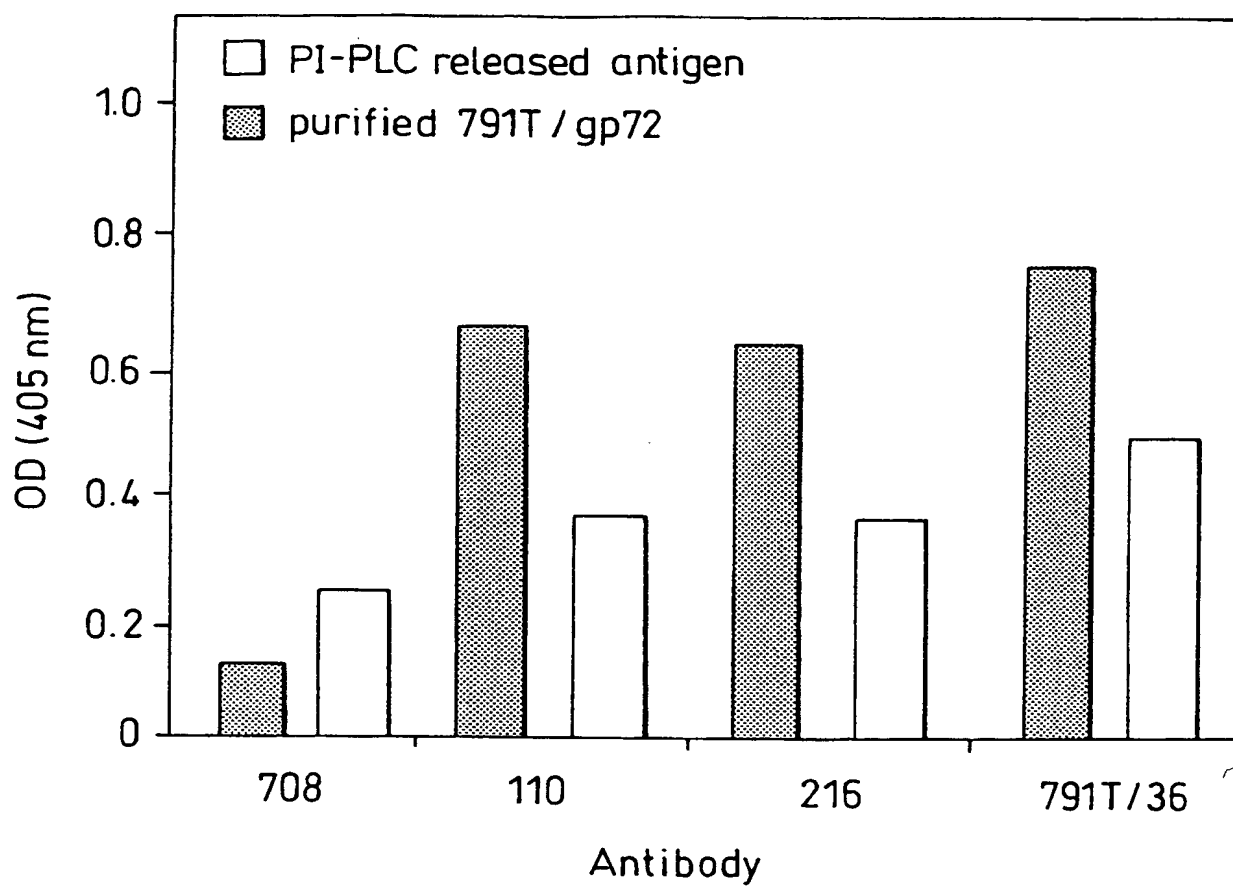
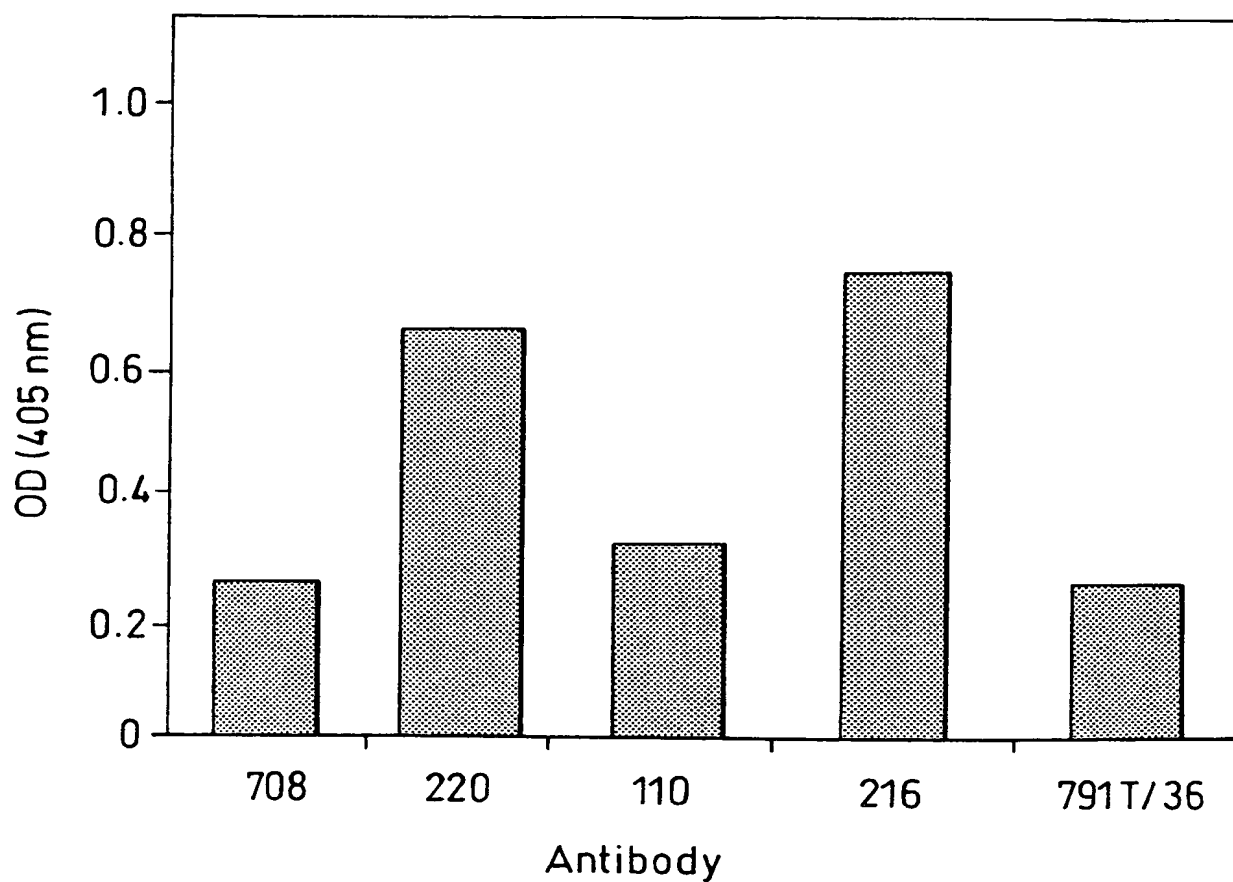


Fig. 5

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**Fig. 6**

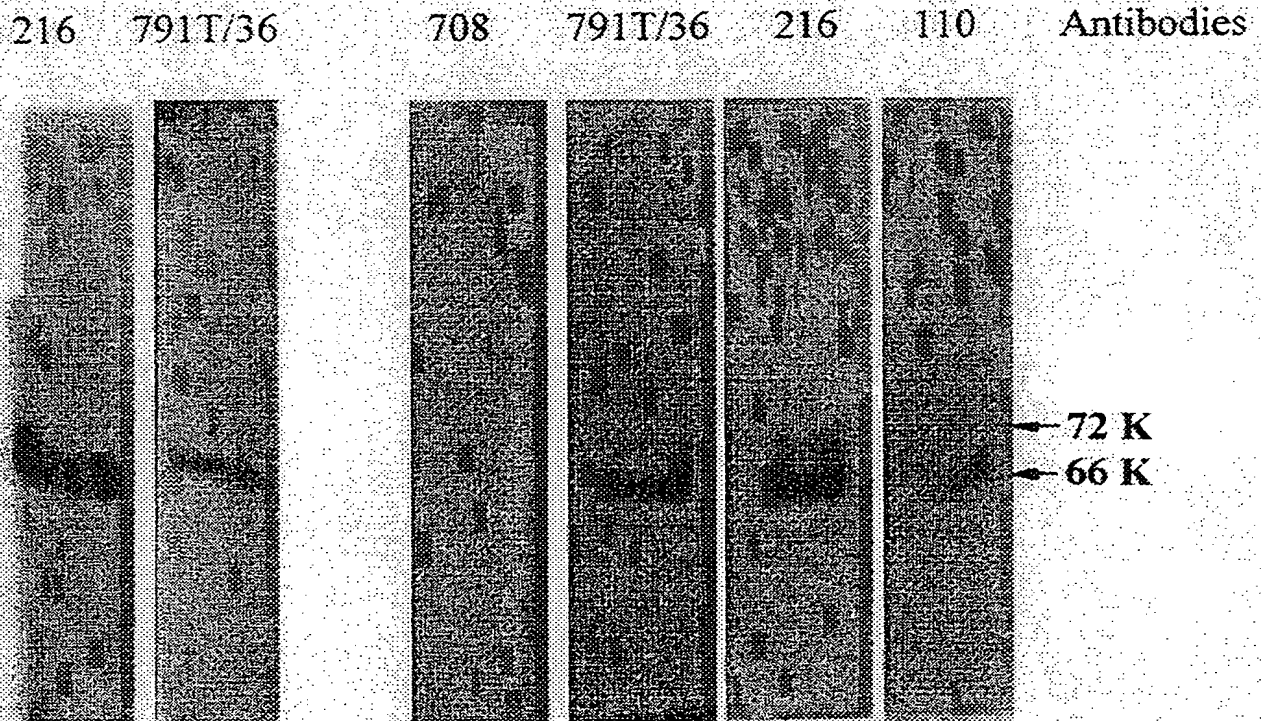
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*Fig. 7*

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Erythrocytes

791T cells

*Fig. 8*

9/23

Age Group	Number of People
10-19	10
20-29	20
30-39	30
40-49	40
50-59	50

5/P5
C-DAF.seq
RC of B/C DAF

CCGCTGGCGTAGCTCGGACTCGGCGGAGTCCCGCGGCGGTCTTGTCTAAACCGG

Year	1960	1970	1980	1990	2000	2010
Population (millions)	1.2	1.5	2.0	2.5	3.0	3.5
GDP (billions of dollars)	100	200	400	800	1500	2500
Life expectancy (years)	45	55	65	70	75	78
Urban population (%)	20	30	45	60	75	85
Healthcare expenditure (GDP %)	2	3	4	5	6	7
Education expenditure (GDP %)	1	1.5	2	2.5	3	3.5
Government expenditure (GDP %)	15	18	22	25	28	30
Private sector contribution (GDP %)	85	82	78	75	72	70
Unemployment rate (%)	5	6	7	8	9	10
Income inequality (Gini index)	0.35	0.38	0.40	0.42	0.45	0.48
Environmental index	10	15	20	25	30	35
Technological innovation index	1	2	3	4	5	6
Globalization index	1	2	3	4	5	6
Human Development Index	0.5	0.6	0.7	0.8	0.9	1.0

5/P5
C-DAF.seq
RC of B/C DAF

GGCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCTGCCCTCCTCGGGAG

Year	1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100																																																																																																																																																									
Population	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413

5/P5
C-DAF. seq
RC of B/C DAF

CTGCCCGGCTGCTGCTGCTGGTGTGTGTGCCCTGCCGGCGGTGTGGGGTGACTGTG

Fig. 9 (part 1 of 11)

10/23

5/P5	180	190	200	210	220	230
C-DAF.seq						
RC of B/C DAF						
	-----GTACAAGTTTCC					
	GCCTTCCCCAGATGTACCTAATGCCAGCCAGCTTTGGAAGCCGTACAAGTTTCC					

5/P5	240	250	260	270	280	290
C-DAF.seq						
RC of B/C DAF						
	CGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAG					
	CGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAG					

5/P5	300	310	320	330	340	
C-DAF.seq						
RC of B/C DAF						
	AAGGACTCAGTGATCTGCCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCA					
	AAGGACTCAGTGATCTGCCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCA					

Fig. 9 (part 2 of 11)

11/23

5/P5	350	360	370	380	390	400
C-DAF.seq						
RC of B/C DAF	-----	-----	-----	-----	-----	-----
	ATCGTAGCTGCGAGGTGCCAACAAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATAT					
	ATCGTAGCTGCGAGGTGCCAACAAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATAT					
	-----	-----	-----	-----	-----	-----
5/P5	410	420	430	440	450	460
C-DAF.seq						
RC of B/C DAF	-----	-----	-----	-----	-----	-----
	CACTCAGAATTATTTCCAGTCGGTACTGTGTGGAATATGAGTGCCGTCAGGTTAC					
	CACTCAGAATTATTTCCAGTCGGTACTGTGTGGAATATGAGTGCCGTCAGGTTAC					
	-----	-----	-----	-----	-----	-----
5/P5	470	480	490	500	510	520
C-DAF.seq						
RC of B/C DAF	-----	-----	-----	-----	-----	-----
	AGAAGAGAACCTTCTCTATCACCAAACAACTAAGTTCAGAAATTTAAATGGTCCA					
	AGAAGAGAACCTTCTCTATCACCAAACAACTAAGTTCAGAAATTTAAATGGTCCA					
	-----	-----	-----	-----	-----	-----
5/P5	530	540	550	560	570	580
C-DAF.seq						
RC of B/C DAF	-----	-----	-----	-----	-----	-----
	CAGCAGTCGAATTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGG					
	CAGCAGTCGAATTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGG					
	-----	-----	-----	-----	-----	-----

Fig. 9 (part 3 of 11)

12/23

5/P5	TCAGATTGATGTACCAGGTGGCATATTATTGATGCAACCATCTCCTTCTCATGTAA	590	600	610	620	630	
C-DAF. seq	TCAGATTGATGTACCAGGTGGCATATTATTGATGCAACCATCTCCTTCTCATGTAA						
RC of B/C DAF	-----TATTATTGNTGCAACCATTTCTCTTTTCATGTAA						
5/P5	CACAGGGTACAAATTATTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTC	640	650	660	670	680	690
C-DAF. seq	CACAGGG-TACAAATTATTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTC						
RC of B/C DAF	CACANGG-TACAAATTATTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTC						
5/P5	TGTCCAGTGGAGTGACCCGTTGCCAGATGCAGAGAAATTA-TGTCCAGCACCACCA	700	710	720	730	740	750
C-DAF. seq	TGTCCAGTGGAGTGACCCGTTGCCAGATGCAGAGAAATTA-TGTCCAGCACCACCA						
RC of B/C DAF	TGTCCAGTGGAGTGACCCGTTGCCAGATGCAGAGAAATTA-TGTCCAGCACCACCA						

Fig. 9 (part 4 of 11)

13/23

5/P5	760	770	780	790	800	810
C-DAF.seq						
RC of B/C DAF						
	CAAATTGACA-TGGAATAATCCAGGGGAACGTTGACCATTTGGATATAAACG-----					
	CAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTTGGATATAGACAGTCTG					
	CAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTTGGATATAGACAGTCTG					
	820	830	840	850	860	870

5/P5	TAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATTATTGTAC					
C-DAF.seq	TAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATTATTGTAC					
RC of B/C DAF						
	880	890	900	910	920	

5/P5	TGTGAATAATGATGAAGGAGAGTGGAGTGGCCCCACCACCTGAATGCAGAGGAAATCT					
C-DAF.seq	TGTGAATAATGATGAAGGAGAGTGGAGTGGCCCCACCACCTGAATGCAGAGGAAATCT					
RC of B/C DAF						

Fig. 9 (part 5 of 11)

14/23

5/P5	930	940	950	960	970	980
C-DAF.seq						
RC of B/C DAF						

	CTAACTCCAAGGTC	CCACCAACAGTT	CAGAAACCT	ACCACAGTAAAT	GTTC	CCAACTA
	CTAACTCCAAGGTC	CCACCAACAGTT	CAGAAACCT	ACCACAGTAAAT	GTTC	CCAACTA
	990	1000	1010	1020	1030	1040

5/P5	1050	1060	1070	1080	1090	1100
C-DAF.seq						
RC of B/C DAF						

	CAGAAGTCTACCA	ACTTCTCAGAA	AAACCA	CAAAACCA	CCACCA	CAAAATGCTCA
	CAGAAGTCTACCA	ACTTCTCAGAA	AAACCA	CAAAACCA	CCACCA	CAAAATGCTCA
	1110	1120	1130	1140	1150	1160

5/P5	1110	1120	1130	1140	1150	1160
C-DAF.seq						
RC of B/C DAF						

	AATAAAGGAAGTG	GAACCACTT	CAGGTACT	ACCCGTCTT	CTATCT	GGGCACACGTGT
	AATAAAGGAAGTG	GAACCACTT	CAGGTACT	ACCCGTCTT	CTATCT	GGGCACACGTGT

Fig. 9 (part 6 of 11)

15/23

5/P5	1170	1180	1190	1200	1210
C-DAF.seq					
RC of B/C DAF					

	TCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGCCAAA				
	TCAC				

	1220	1230	1240	1250	1260

	GAAGAGTTAAGAAGAAAAATACACACAAGTATACAGACTGTTCCCTAGTTTCTTAGACTT				

	1280	1290	1300	1310	1320

	ATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTAGGATGCTTTCATTG				

5/P5	1280	1290	1300	1310	1330
C-DAF.seq					
RC of B/C DAF					

Fig. 9 (part 7 of 11)

16/23

5/P5	1340	1350	1360	1370	1380	1390
C-DAF.seq						
RC of B/C DAF	-----	-----	-----	-----	-----	-----
	TCTTTAAGATGTGTAGGAATGTCAACAGAGCAAGGAGAAAAAGGCAGTCCTGGAAT					
	-----	-----	-----	-----	-----	-----
5/P5	1400	1410	1420	1430	1440	1450
C-DAF.seq						
RC of B/C DAF	-----	-----	-----	-----	-----	-----
	CACATTCTTAGCACACCTACACCTCTTGAAAAATAGAACAACTTGCAGAATTGAGAGTG					
	-----	-----	-----	-----	-----	-----
5/P5	1460	1470	1480	1490	1500	
C-DAF.seq						
RC of B/C DAF	-----	-----	-----	-----	-----	-----
	ATTCCTTTCCTAAAGTGTAAAGAACATAGAGATTGTTCGTATTAGAAATGGGATC					
	-----	-----	-----	-----	-----	-----

Fig. 9 (part 8 of 11)

17/23

5/P5	1510	1520	1530	1540	1550	1560
C-DAF.seq						
RC of B/C DAF						

	ACGAGGAAAAGAGAAGGAAAGTGATTTTTTCCACAAGATCTGTAATGTTATTCCAC					

	1570	1580	1590	1600	1610	1620

	TTATAAGGAAATAAAAAATGAAAAACATTATTGGATATCAAAAGCAAAATAAAACC					

	1630	1640	1650	1660	1670	1680

	CAATTCAGTCTCTTCTAAGCAAATTGCTAAAGAGAGATGAACCATTTATAAAGTAA					

	1690	1700	1710	1720	1730	1740

	TCTTTGGCTGAAGGCATTTTCATCTTTCCTCGGGTTGGCAAAATATTTTAAAGGTA					

5/P5	1690	1700	1710	1720	1730	1740
C-DAF.seq						
RC of B/C DAF						

	TCTTTGGCTGAAGGCATTTTCATCTTTCCTCGGGTTGGCAAAATATTTTAAAGGTA					

Fig. 9 (part 9 of 11)

18/23

5/P5
C-DAF.seq
RC of B/C DAF

AAACATGCTGGTGAACCAGGGGTGTTGATGGTGATAAGGAGGAATATAGAATGAAAG

1750 1760 1770 1780 1790
| | | | |

5/P5
C-DAF.seq
RC of B/C DAF

ACTGAATCTTCCTTGTTCACAAATAGAGTTGGAAAAAGCCTGTGAAAGGTGTCTT

1800 1810 1820 1830 1840 1850
| | | | |

5/P5
C-DAF.seq
RC of B/C DAF

CTTGACTTAATGTCTTTAAAGTATCCAGAGATACTACAATATTAAACATAAGAAAG

1860 1870 1880 1890 1900 1910
| | | | |

5/P5
C-DAF.seq
RC of B/C DAF

ATTATATATTCTGAATCGAGATGCCATAGTCAAATTTGTAAATCTTATTCTTT

1920 1930 1940 1950 1960 1970
| | | | |

Fig. 9 (part 10 of 11)

19/23

1980 1990 2000 2010 2020 2030
| | | | | |

5/P5
C-DAF.seq
RC of B/C DAF

TGTAATATTATTATTTATTATGACAGTGAACATTCTGATTTTACATGTAAAC

2040 2050 2060 2070 2080
| | | | |

5/P5
C-DAF.seq
RC of B/C DAF

AAGAAAAGTTGAAGAAGATATGTGAAGAAAAATGTATTTTCCTAAATAGAAATAAT

2090 2100
| |

5/P5
C-DAF.seq
RC of B/C DAF

-----T
GATCCCATTTTGGT

Fig. 9 (part 11 of 11)

20/23

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1                                     CC GCT GGG CGT AGC
15  TGC GAC TCG GCG GAG TCC CGG CGG CGC GTC CTT GTT CTA ACC CGG CGC GCC
    |<-- Leader sequence
    Met Thr Val Ala Arg Pro Ser Val Pro Ala Ala Leu Pro Leu Leu Gly Glu 17
66  ATG ACC GTC GCG CGG CCG AGC GTG CCC GCG GCG CTG CCC CTC CTC GGG GAG
    Leu Pro Arg Leu Leu Leu Leu Val Leu Leu Cys Leu Pro Ala Val Trp Gly 34
117 CTG CCC CGG CTG CTG CTG CTG GTG CTG TTG TGC CTG CCG GCC GTG TGG GGT
    <- sushi 1
    |<-- mature sequence (first 16 amino acids sequenced)
    Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala Leu Glu Gly 51
168 GAC TGT GGC CTT CCC CCA GAT GTA CCT AAT GCC CAG CCA GCT TTG GAA GGC
    Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys Cys Glu Glu Ser 68
219 CGT ACA AGT TTT CCC GAG GAT ACT GTA ATA ACG TAC AAA TGT GAA GAA AGC
    Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Ile Cys Leu Lys Gly Ser 85
270 TTT GTG AAA ATT CCT GGC GAG AAG GAC TCA GTG ATC TGC CTT AAG GGC AGT
    sushi 1 ->| |sushi 2
    Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg Ser Cys Glu Val Pro Thr 102
321 CAA TGG TCA GAT ATT GAA GAG TTC TGC AAT CGT AGC TGC GAG GTG CCA ACA
    Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro Tyr Ile Thr Gln Asn Tyr Phe 119
372 AGG CTA AAT TCT GCA TCC CTC AAA CAG CCT TAT ATC ACT CAG AAT TAT TTT
    Pro Val Gly Thr Val Val Glu Tyr Glu Cys Arg Pro Gly Tyr Arg Arg Glu 136
423 CCA GTC GGT ACT GTT GTG GAA TAT GAG TGC CGT CCA GGT TAC AGA AGA GAA
    Pro Ser Leu Ser Pro Lys Leu Thr Cys Leu Gln Asn Leu Lys Trp Ser Thr 153
474 CCT TCT CTA TCA CCA AAA CTA ACT TGC CTT CAG AAT TTA AAA TGG TCC ACA
    sushi 2 ->| |<- sushi 3
    Ala Val Glu Phe Cys Lys Lys Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg 170
525 GCA GTC GAA TTT TGT AAA AAG AAA TCA TGC CCT AAT CCG GGA GAA ATA CGA
    Asn Gly Gln Ile Asp Val Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser 187
576 AAT GGT CAG ATT GAT GTA CCA GGT GGC ATA TTA TTT GGT GCA ACC ATC TCC
    Phe Ser Cys Asn Thr Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys 204
627 TTC TCA TGT AAC ACA GGG TAC AAA TTA TTT GGC TCG ACT TCT AGT TTT TGT
    sushi 3 ->|
    Leu Ile Ser Gly Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg 221
678 CTT ATT TCA GGC AGC TCT GTC CAG TGG AGT GAC CCG TTG CCA GAG TGC AGA
    |<- sushi 4
    Glu Ile Tyr Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly 238
729 GAA ATT TAT TGT CCA GCA CCA CCA CAA ATT GAC AAT GGA ATA ATT CAA GGC

```

Fig. 10 (part 1 of 2)

21/23

780 Glu Arg Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys 255
 GAA CGT GAC CAT TAT GGA TAT AGA CAG TCT GTA ACG TAT GCA TGT AAT AAA
 831 Gly Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp 272
 GGA TTC ACC ATG ATT GGA GAG CAC TCT ATT TAT TGT ACT GTG AAT AAT GAT
 sushi 4->|
 885 Glu Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Gly Lys Ser Leu Thr 289
 GAA GGA GAG TGG AGT GGC CCA CCA CCT GAA TGC AGA GGA AAA TCT CTA ACT
 933 Ser Lys Val Pro Pro Thr Val Gln Lys Pro Thr Thr Val Asn Val Pro Thr 306
 TCC AAG GTC CCA CCA ACA GTT CAG AAA CCT ACC ACA GTA AAT GTT CCA ACT
 984 Thr Glu Val Ser Pro Thr Ser Gln Lys Thr Thr Thr Lys Thr Thr Thr Pro 323
 ACA GAA GTC TCA CCA ACT TCT CAG AAA ACC ACC ACA AAA ACC ACC ACA CCA
 1035 Asn Ala Gln Ala Thr Arg Ser Thr Pro Val Ser Arg Thr Thr Lys His Phe 340
 AAT GCT CAA GCA ACA CGG AGT ACA CCT GTT TCC AGG ACA ACC AAG CAT TTT
 1086 His Glu Thr Thr Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg 357
 CAT GAA ACA ACC CCA AAT AAA GGA AGT GGA ACC ACT TCA GGT ACT ACC CGT
 1137 Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu 374
 CTT CTA TCT GGG CAC ACG TGT TTC ACG TTG ACA GGT TTG CTT GGG ACG CTA
 1188 Val Thr Met Gly Leu Leu Thr Stop 381
 GTA ACC ATG GGC TTG CTG ACT TAG CCAAAGAAGAGTTAAGAAG
 1231 AAAATACACACAAGTATACAGACTGTTCTTAGTTTCTTAGACTTATCTGCATATTGGATAAAATAAA
 1298 TGCAATTGTGCTCTTCATTTAGGATGCTTTTATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGC
 1365 AAGGAGAAAAAAGGCAGTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAAC
 1432 TTGCAGAATTGAGAGTGATTCTTTCTTAAAGTGTAAGAAAAGCATAGAGATTTGTTTCGTATTTAGA
 1499 ATGGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTTCCACT
 1566 TATAAAGGAAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAACCCAATTCAGTC
 1633 TCTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAATCTTTGGCTGTAAGGCATT
 1700 TTCATCTTTCTTCGGGTTGGCAAAATATTTTAAAGGTAAAAACATGCTGGTGAACCAGGGGTGTTGA
 1767 TGGTGATAAGGGAGGAATATAGAATGAAAGACTGAATCTTCCTTTGTTGCACAAATAGAGTTTGGAA
 1834 AAAGCCTGTGAAAGGTGCTTTCTTTGACTTAATGTCTTTTAAAGTATCCAGAGATACTACAATATTA
 1901 ACATAAGAAAAGATTATATATTATTTCTGAATCGAGATGTCCATAGTCAAATTTGTAAATCTTATTC
 1968 TTTTGTAATATTTATTTATATTTATTTATGACAGTGAACATTCTGATTTTACATGTAAAACAAGAAA
 2035 AGTTGAAGAAGATATGTGAAGAAAATGTATTTTTCTTAAATAGAAATAAATGATCCCATTTTTTGG
 2102 T

Fig. 10 (part 2 of 2)

22/23

1 TTTAAACGGGCCCTCTAGACTCGAGCGGCCGCTGCCCATCTTGTCGTCGTCGTCCTTG TAGTCG
 65 TGCATGTGGTGGTGGTGGTGGTGGTTAACCATGGTGGCGGGCCGCCACTGTGCTGGATATCTGCAGA
 132 ATTCGATGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCC

Met Thr Val Ala Arg Pro Ser Val Pro Ala Ala Leu Pro Leu Leu Gly Glu 17
 199 ATG ACC GTC GCG CGG CCG AGC GTG CCC GCG GCG CTG CCC CTC CTC GGG GAG

Leu Pro Arg Leu Leu Leu Leu Val Leu Leu Cys Leu Pro Ala Val Trp Gly 34
 250 CTG CCC CGG CTG CTG CTG CTG GTG CTG TTG TGC CTG CCG GCC GTG TGG GGT

Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala Leu Glu Gly 51
 301 GAC TGT GGC CTT CCC CCA GAT GTA CCT AAT GCC CAG CCA GCT TTG GAA GGC

Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys Cys Glu Glu Ser 68
 352 CGT ACA AGT TTT CCC GAG GAT ACT GTA ATA ACG TAC AAA TGT GAA GAA AGC

Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Ile Cys Leu Lys Gly Ser 85
 403 TTT GTG AAA ATT CCT GGC GAG AAG GAC TCA GTG ATC TGC CTT AAG GGC AGT

Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg Ser Cys Glu Val Pro Thr 102
 454 CAA TGG TCA GAT ATT GAA GAG TTC TGC AAT CGT AGC TGC GAG GTG CCA ACA

Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro Tyr Ile Thr Gln Asn Tyr Phe 119
 505 AGG CTA AAT TCT GCA TCC CTC AAA CAG CCT TAT ATC ACT CAG AAT TAT TTT

Pro Val Gly Thr Val Val Glu Tyr Glu Cys Arg Pro Gly Tyr Arg Arg Glu 136
 556 CCA GTC GGT ACT GTT GTG GAA TAT GAG TGC CGT CCA GGT TAC AGA AGA GAA

Pro Ser Leu Ser Pro Lys Leu Thr Cys Leu Gln Asn Leu Lys Trp Ser Thr 153
 607 CCT TCT CTA TCA CCA AAA CTA ACT TGC CTT CAG AAT TTA AAA TGG TCC ACA

Ala Val Glu Phe Cys Lys Lys Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg 170
 658 GCA GTC GAA TTT TGT AAA AAG AAA TCA TGC CCT AAT CCG GGA GAA ATA CGA

Asn Gly Gln Ile Asp Val Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser 187
 709 AAT GGT CAG ATT GAT GTA CCA GGT GGC ATA TTA TTT GGT GCA ACC ATC TCC

Phe Ser Cys Asn Thr Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys 204
 760 TTC TCA TGT AAC ACA GGG TAC AAA TTA TTT GGC TCG ACT TCT AGT TTT TGT

Fig. 11 (part 1 of 2)

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Leu Ile Ser Gly Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg 221
 811 CTT ATT TCA GGC AGC TCT GTC CAG TGG AGT GAC CCG TTG CCA GAG TGC AGA

Glu Ile Tyr Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly 238
 862 GAA ATT TAT TGT CCA GCA CCA CCA CAA ATT GAC AAT GGA ATA ATT CAA GGG

Glu Arg Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys 255
 913 GAA CGT GAC CAT TAT GGA TAT AGA CAG TCT GTA ACG TAT GCA TGT AAT AAA

Gly Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp 272
 964 GGA TTC ACC ATG ATT GGA GAG CAC TCT ATT TAT TGT ACT GTG AAT AAT GAT

Glu Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Gly Lys Ser Leu Thr 289
 1015GAA GGA GAG TGG AGT GGC CCA CCA CCT GAA TGC AGA GGA AAA TCT CTA ACT

Ser Lys Val Pro Pro Thr Val Gln Lys Pro Thr Thr Val Asn Val Pro Thr 306
 1066TCC AAG GTC CCA CCA ACA GTT CAG AAA CCT ACC ACA GTA AAT GTT CCA ACT

Thr Glu Val Ser Pro Thr Ser Gln Lys Thr Thr Thr Lys Thr Thr Thr Pro 323
 1117ACA GAA GTC TCA CCA ACT TCT CAG AAA ACC ACC ACA AAA ACC ACC ACA CCA

Asn Ala Gln Ala Thr Arg Ser Thr Pro Val Ser Arg Thr Thr Lys His Phe 340
 1168AAT GCT CAA GCA ACA CGG AGT ACA CCT GTT TCC AGG ACA ACC AAG CAT TTT

His Glu Thr Thr Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg 357
 1219CAT GAA ACA ACC CCA AAT AAA GGA AGT GGA ACC ACT TCA GGT ACT ACC CGT

Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu 374
 1270CTT CTA TCT GGG CAC ACG TGT TTC ACG TTG ACA GGT TTG CTT GGG ACG CTA

Val Thr Met Gly Leu Leu Thr Stop 381
 1321GTA ACC ATG GGC TTG CTG ACT TAG CCAAAGAAGAGTTAAGAAGAAAATACACACAAGTA

1380TACAGACTGTTCTAGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTC
 1447ATTTAGGATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA

Fig. 11 (part 2 of 2)